

GCTATTGTCG	ACGTATGACG	TTTGCTCTAT	AGCCATCGCT	GCTCCCATGC	GCGCCACTCG	60
GTGCGAGGGG	GTGTGGGATT	TTTTTTGGGA	GACAATCCTC	ATGGCCTATA	CGACGGCCCA	120
GTTGGTGACT	GCGTACACCA	ACGCCAACCT	CGGCAAGGCG	CCTGACGCCG	CCACCACGCT	180
GACGCTCGAC	GCGTACGCGA	CTCAAACCCA	GACGGGCGGC	CTCTCGGACG	CCGCTGCGCT	240
GACCAACACC	CTGAAGCTGG	TCAACAGCAC	GACGGCTGTT	GCCATCCAGA	CCTACCAGTT	300
CTTCACCGGC	GTTGCCCGGT	CGGCCGCTGG	TCTGGACTTC	CTGGTCGACT	CGACCACCAA	360
CACCAACGAC	CTGAACGACG	CGTACTACTC	GAAGTTCGCT	CAGGAAAACC	GCTTCATCAA	420
CTTCTCGATC	AACCTGGCCA	CGGGCGCCGG	CGCCGGCGCG	ACGGCTTTCG	CCGCCGCCCTA	480
CACGGGCGTT	TCGTACGCCC	AGACGGTCGC	CACCGCCTAT	GACAAGATCA	TCGGCAACGC	540
CGTCGCGACC	GCCGCTGGCG	TCGACGTGCG	GGCCGCCGTG	GCTTTCCTGA	GCCGCCAGGC	600
CAACATCGAC	TACCTGACCG	CCTTCGTGCG	CGCCAACACG	CCGTTACGG	CCGCTGCCGA	660
CATCGATCTG	GCCGTCAAGG	CCGCCCTGAT	CGGCACCATC	CTGAACGCCG	CCACGGTGTC	720
GGGCATCGGT	GGTTACGCGA	CCGCCACGGC	CGCGATGATC	AACGACCTGT	CGGACGGCGC	780
CCTGTCGACC	GACAACGCGG	CTGGCGTGAA	CCTGTTTACC	GCCTATCCGT	CGTCGGGCGT	840
GTCGGGTTCG	ACCCCTCTCG	TGACCACCGG	CACCGACACC	CTGACGGGCA	CCGCCAACAA	900
CGACACGTTT	GTTGCGGGTG	AAGTCGCCCG	CGCTGCGACC	CTGACCGTTG	GCGACACCCT	960
GAGCGGCGGT	GCTGGCACCG	ACGTCCTGAA	CTGGGTGCAA	GCTGCTGCGG	TTACGGCTCT	1020
GCCGACCGGC	GTGACGATCT	CGGGCATCGA	AACGATGAAC	GTGACGTCGG	GCGCTGCGAT	1080
CACCCTGAAC	ACGCTTTCGG	GCGTGACGGG	TCTGACCGCC	CTGAACACCA	ACACCAGCGG	1140
CGCGGCTCAA	ACCGTCACCG	CCGGCGCTGG	CCAGAACCTG	ACCGCCACGA	CCGCCGCTCA	1200
AGCCGCGAAC	AACGTCGCCG	TCGACGGGCG	CGCCAACGTC	ACCGTCGCCT	CGACGGGCGT	1260
GACCTCGGGC	ACGACCACGG	TCGGCGCCAA	CTCGGCCGCT	TCGGGCACCG	TGTCGGTGAG	1320
CGTCGCGAAC	TCGAGCACGA	CCACCACGGG	CGCTATCGCC	GTGACCGGTG	GTACGGCCGT	1380
GACCGTGGCT	CAAACGGCCG	GCAACGCCGT	GAACACCACG	TTGACGCAAG	CCGACGTGAC	1440
CGTGACCGGT	AACTCCAGCA	CCACGGCCGT	GACGGTCACC	CAAACGCCCG	CCGCCACCGC	1500
CGGGCGTACG	GTCGCCGGTC	GCGTCAACGG	CGCTGTGACG	ATCACCGACT	CTGCCGCCGC	1560
CTCGGCCACG	ACCGCCGGCA	AGATCGCCAC	GGTCACCCTG	GGCAGCTTCG	GCGCCGCCAC	1620
GATCGACTCG	AGCGCTCTGA	CGACCGTCAA	CCTGTCGGGC	ACGGGCACCT	CGCTCGGCAT	1680

20
Appendix 1 (cont'd)

CGGCCGCGGC GCTCTGACCG CCACGCCGAC CGCCAACACC CTGACCCTGA ACGTCAATGG 1740
TCTGACGACG ACCGGCGCGA TCACGGACTC GGAAGCGGCT GCTGACGATG GTTTCACCAC 1800
CATCAACATC GCTGGTTTGA CCGCCTCTTC GACGATCGCC AGCCTGGTGG CCGCCGACGC 1860
GACGACCCTG AACATCTCGG GCGACGCTCG CGTCACGATC ACCTCGCACA CCGCTGCCGC 1920
CCTGACGGGC ATCACGGTGA CCAACAGCGT TGGTGCGACC CTCGGCGCCG AACTGGCGAC 1980
CGGTCTGGTC TTCACGGGCG GCGCTGGCCG TGA CTCGATC CTGCTGGGCG CCACGACCAA 2040
GGCGATCGTC ATGGGCGCCG GCGACGACAC CGTCACCGTC AGCTCGGCGA CCCTGGGCGC 2100
TGGTGGTTTG GTCAACGGCG GCGACGGCAC CGACGTTCTG GTGGCCAACG TCAACGGTTC 2160
GTCGTTTACG GCTGACCCGG CTTTCGGCGG CTTGAAACC CTCGCGTCG CTGGCGCGGC 2220
GGCTCAAGGC TCGCACAACG CCAACGGCTT CACGGCTCTG CAACTGGGCG CGACGGCGGG 2280
TGCGACGACC TTCACCAACG TTGCGGTGAA TGTCGGCCTG ACCGTTCTGG CGGCTCCGAC 2340
CGGTACGACG ACCGTGACCC TGGCCAACGC CACGGGCACC TCGGACGTGT TCAACCTGAC 2400
CCTGTCTGTC TCGGCGGCTC TGGCCGCTGG TACGGTTGCG CTGGCTGGCG TCGAGACGGT 2460
GAACATCGCC GGCACCGACA CCAACACGAC CGCTCACGTC GACACGCTGA CGCTGCAAGC 2520
CACCTCGGCC AAGTCGATCG TGGTGACGGG CAACGCCGGT CTGAACCTGA CCAACACCGG 2580
CAACACGGCT GTCACCACT TCGACGCCAG CGCCGTCACC GGCACGGCTC CGGCTGTGAC 2640
CTTCGTGTCTGCCAACACCA CCGTGGGTGA AGTCGTCACG ATCCGCGGCG GCGCTGGCGC 2700
CGACTCGCTG ACCGGTTCTGG CCACCGCCAA TGACACCATC ATCGGTGGCG CTGGCGCTGA 2760
CACCTGGTTC TACACCGGCG GTACGGACAC CTTACGGGT GGCACGGGCG CGGATATCTT 2820
CGATATCAAC GCTATCGGCA CCTCGACCGC TTTCGTGACG ATCACCAGC CCGCTGTCTG 2880
CGACAAGCTC GACCTCGTCG GCATCTCGAC GAACGGCGCT ATCGCTGACG GCGCCTTCGG 2940
CGCTGCGGTC ACCCTGGGCG CTGCTGCGAC CCTGGCTCAG TACCTGGACG CTGCTGCTGC 3000
CGGCGACGGC AGCGGCACCT CGGTTGCCAA GTGGTTCCAG TTCGGCGGCG ACACCTATGT 3060
CGTCGTTGAC AGCTCGGCTG GCGCGACCTT CGTCAGCGGC GCTGACGCGG TGATCAAGCT 3120
GACCGGTCTG GTCACGCTGA CCACCTCGGC CTTGCCACC GAAGTCCTGA CGCTCGCCTA 3180
AGCGAACGTC TGATCCTCGC CTAGGCGAGG ATCGCTAGAC TAAGAGACCC CGTCTTCCGA 3240
AAGGGAGGCG GGGTCTTTCT TATGGGCGCT ACGCGCTGGC CGGCCTTGCC TAGTTCCGGT 3300

FIG. 10

21
Appendix 1 (cont'd)

Met Ala Tyr Thr Thr Ala Gln Leu Val Thr Ala Tyr Thr Asn Ala Asn
1 5 10 15

Leu Gly Lys Ala Pro Asp Ala Ala Thr Thr Leu Thr Leu Asp Ala Tyr
20 25 30

Ala Thr Gln Thr Gln Thr Gly Gly Leu Ser Asp Ala Ala Ala Leu Thr
35 40 45

Asn Thr Leu Lys Leu Val Asn Ser Thr Thr Ala Val Ala Ile Gln Thr
50 55 60

Tyr Gln Phe Phe Thr Gly Val Ala Pro Ser Ala Ala Gly Leu Asp Phe
65 70 75 80

Leu Val Asp Ser Thr Thr Asn Thr Asn Asp Leu Asn Asp Ala Tyr Tyr
85 90 95

Ser Lys Phe Ala Gln Glu Asn Arg Phe Ile Asn Phe Ser Ile Asn Leu
100 105 110

Ala Thr Gly Ala Gly Ala Gly Ala Thr Ala Phe Ala Ala Ala Tyr Thr
115 120 125

Gly Val Ser Tyr Ala Gln Thr Val Ala Thr Ala Tyr Asp Lys Ile Ile
130 135 140

Gly Asn Ala Val Ala Thr Ala Ala Gly Val Asp Val Ala Ala Ala Val
145 150 155 160

Ala Phe Leu Ser Arg Gln Ala Asn Ile Asp Tyr Leu Thr Ala Phe Val
165 170 175

Arg Ala Asn Thr Pro Phe Thr Ala Ala Ala Asp Ile Asp Leu Ala Val
180 185 190

Lys Ala Ala Leu Ile Gly Thr Ile Leu Asn Ala Ala Thr Val Ser Gly
195 200 205

Ile Gly Gly Tyr Ala Thr Ala Thr Ala Ala Met Ile Asn Asp Leu Ser
210 215 220

Asp Gly Ala Leu Ser Thr Asp Asn Ala Ala Gly Val Asn Leu Phe Thr
225 230 235 240

Ala Tyr Pro Ser Ser Gly Val Ser Gly Ser Thr Leu Ser Leu Thr Thr
245 250 255

Gly Thr Asp Thr Leu Thr Gly Thr Ala Asn Asn Asp Thr Phe Val Ala
260 265 270

Gly Glu Val Ala Gly Ala Ala Thr Leu Thr Val Gly Asp Thr Leu Ser
275 280 285

Gly Gly Ala Gly Thr Asp Val Leu Asn Trp Val Gln Ala Ala Ala Val
290 295 300

Thr Ala Leu Pro Thr Gly Val Thr Ile Ser Gly Ile Glu Thr Met Asn
305 310 315 320

Val Thr Ser Gly Ala Ala Ile Thr Leu Asn Thr Ser Ser Gly Val Thr
325 330 335

Gly Leu Thr Ala Leu Asn Thr Asn Thr Ser Gly Ala Ala Gln Thr Val
340 345 350

22
Appendix 1 (cont'd)

Thr Ala Gly Ala Gly Gln Asn Leu Thr Ala Thr Thr Ala Ala Gln Ala
355 360 365

Ala Asn Asn Val Ala Val Asp Gly Arg Ala Asn Val Thr Val Ala Ser
370 375 380

Thr Gly Val Thr Ser Gly Thr Thr Thr Val Gly Ala Asn Ser Ala Ala
385 390 395 400

Ser Gly Thr Val Ser Val Ser Val Ala Asn Ser Ser Thr Thr Thr Thr
405 410 415

Gly Ala Ile Ala Val Thr Gly Gly Thr Ala Val Thr Val Ala Gln Thr
420 425 430

Ala Gly Asn Ala Val Asn Thr Thr Leu Thr Gln Ala Asp Val Thr Val
435 440 445

Thr Gly Asn Ser Ser Thr Thr Ala Val Thr Val Thr Gln Thr Ala Ala
450 455 460

Ala Thr Ala Gly Ala Thr Val Ala Gly Arg Val Asn Gly Ala Val Thr
465 470 475 480

Ile Thr Asp Ser Ala Ala Ala Ser Ala Thr Thr Ala Gly Lys Ile Ala
485 490 495

Thr Val Thr Leu Gly Ser Phe Gly Ala Ala Thr Ile Asp Ser Ser Ala
500 505 510

Leu Thr Thr Val Asn Leu Ser Gly Thr Gly Thr Ser Leu Gly Ile Gly
515 520 525

Arg Gly Ala Leu Thr Ala Thr Pro Thr Ala Asn Thr Leu Thr Leu Asn
530 535 540

Val Asn Gly Leu Thr Thr Thr Gly Ala Ile Thr Asp Ser Glu Ala Ala
545 550 555 560

Ala Asp Asp Gly Phe Thr Thr Ile Asn Ile Ala Gly Ser Thr Ala Ser
565 570 575

Ser Thr Ile Ala Ser Leu Val Ala Ala Asp Ala Thr Thr Leu Asn Ile
580 585 590

Ser Gly Asp Ala Arg Val Thr Ile Thr Ser His Thr Ala Ala Ala Leu
595 600 605

Thr Gly Ile Thr Val Thr Asn Ser Val Gly Ala Thr Leu Gly Ala Glu
610 615 620

Leu Ala Thr Gly Leu Val Phe Thr Gly Gly Ala Gly Arg Asp Ser Ile
625 630 635 640

Leu Leu Gly Ala Thr Thr Lys Ala Ile Val Met Gly Ala Gly Asp Asp
645 650 655

Thr Val Thr Val Ser Ser Ala Thr Leu Gly Ala Gly Gly Ser Val Asn
660 665 670

Gly Gly Asp Gly Thr Asp Val Leu Val Ala Asn Val Asn Gly Ser Ser
675 680 685

Phe Ser Ala Asp Pro Ala Phe Gly Gly Phe Glu Thr Leu Arg Val Ala
690 695 700

FOIA b7E

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Appendix 1. (cont'd)

Gly Ala Ala Ala Gln Gly Ser His Asn Ala Asn Gly Phe Thr Ala Leu
705 710 715 720

Gln Leu Gly Ala Thr Ala Gly Ala Thr Thr Phe Thr Asn Val Ala Val
725 730 735

Asn Val Gly Leu Thr Val Leu Ala Ala Pro Thr Gly Thr Thr Thr Val
740 745 750

Thr Leu Ala Asn Ala Thr Gly Thr Ser Asp Val Phe Asn Leu Thr Leu
755 760 765

Ser Ser Ser Ala Ala Leu Ala Ala Gly Thr Val Ala Leu Ala Gly Val
770 775 780

Glu Thr Val Asn Ile Ala Ala Thr Asp Thr Asn Thr Thr Ala His Val
785 790 795 800

Asp Thr Leu Thr Leu Gln Ala Thr Ser Ala Lys Ser Ile Val Val Thr
805 810 815

Gly Asn Ala Gly Leu Asn Leu Thr Asn Thr Gly Asn Thr Ala Val Thr
820 825 830

Ser Phe Asp Ala Ser Ala Val Thr Gly Thr Ala Pro Ala Val Thr Phe
835 840 845

Val Ser Ala Asn Thr Thr Val Gly Glu Val Val Thr Ile Arg Gly Gly
850 855 860

Ala Gly Ala Asp Ser Leu Thr Gly Ser Ala Thr Ala Asn Asp Thr Ile
865 870 875 880

Ile Gly Gly Ala Gly Ala Asp Thr Leu Val Tyr Thr Gly Gly Thr Asp
885 890 895

Thr Phe Thr Gly Gly Thr Gly Ala Asp Ile Phe Asp Ile Asn Ala Ile
900 905 910

Gly Thr Ser Thr Ala Phe Val Thr Ile Thr Asp Ala Ala Val Gly Asp
915 920 925

Lys Leu Asp Leu Val Gly Ile Ser Thr Asn Gly Ala Ile Ala Asp Gly
930 935 940

Ala Phe Gly Ala Ala Val Thr Leu Gly Ala Ala Ala Thr Leu Ala Gln
945 950 955 960

Tyr Leu Asp Ala Ala Ala Ala Gly Asp Gly Ser Gly Thr Ser Val Ala
965 970 975

Lys Trp Phe Gln Phe Gly Gly Asp Thr Tyr Val Val Val Asp Ser Ser
980 985 990

Ala Gly Ala Thr Phe Val Ser Gly Ala Asp Ala Val Ile Lys Leu Thr
995 1000 1005

Gly Leu Val Thr Leu Thr Thr Ser Ala Phe Ala Thr Glu Val Leu Thr
1010 1015 1020

Leu Ala
1025

24
Appendix 2

GAA TTC AGA TCT CAG GGC GCG GGG CAG GGT GGC TAT GGT GGG CTC GGC
TCG CAA GGC
GCT
E F R S Q G A G Q G G Y G G L G S Q G A
GGC CTG GGT GGC CAG GGC GCT GGC GCG GCC GCG GCC GCT GCG GCC GGT
GGC
G R G G Q G A G A A A A A A A G G
GCT GGC CAG GGC GGG CTG GGC TCG CAG GGC GCC GGC CAA GGC GCT GGC
GCC GCG GCC
GCT
A G Q G G L G S Q G A G Q G A G A A A A
GCG GCC GGT GGC GCC GGC CAG GGT GGC TAC GGC GGC CTG GGC AGC CAG
GGC GCC GGT
CGC
A A G G A G Q G G Y G G L G S Q G A G R
GGC GGT CAG GGC GCC GGT GCC GCG GCC GCT GCG GCC GGT GGC GCT GGG
CAA GGC GGC TAC
G G Q G A G A A A A A A G G A G Q G G Y
GGC GGT CTG GGA TCC
G G L G S

Appendix 3

1/1

atg aac aca aac aag gca acc gca act tac ttg aaa tcc att atg ctt cca gag acc
gga
Met asn thr asn lys ala thr ala thr tyr leu lys ser ile met leu pro glu thr
gly
61/21

cca gca agc atc ccg gac gac ata acg gag aga cac atc tta aaa caa gag acc tgg
tca
pro ala ser ile pro asp asp ile thr glu arg his ile leu lys gln glu thr ser
ser
121/41

tac aac tta gag gtc tcc gaa tca gga agt ggc att ctt gtt tgt ttc cct ggg gca
cca
tyr asn leu glu val ser glu ser gly ser gly ile leu val cys phe pro gly ala
pro
181/61

ggc tca cgg atc ggt gca cac tac aga tgg aat grg aac cag acg ggg ctg gag ttc
gac
gly ser arg ile gly ala his tyr arg trp asn ala asn gln thr gly leu glu phe
asp
241/81

cag tgg ctg gag acg tgg cag gac ctg aag aaa gcc ttc aac tac ggg agg ctg atc
tca
gln trp leu glu thr ser gln asp leu lys lys ala phe asn tyr gly arg leu ile
ser
301/101

agg aaa tac gac att caa agc tcc aca cta ccg gcc ggt ctc tat gct ctg aac ggg
acg
arg lys tyr asp ile gln ser ser thr leu pro ala gly leu tyr ala leu asn gly
thr
361/121

ctc aac gct gcc acc ttc gaa ggc agt ctg tct gag gtg gag agc ctg acc tac aat
agc
leu asn ala ala thr phe glu gly ser leu ser glu val glu ser leu thr tyr asn
ser
421/141

ctg atg tcc cta act acg aac ccc cag gac aaa gcc aac aac cag ctg gtg acc aaa
gga
leu met ser leu thr thr asn pro gln asp lys ala asn asn gln leu val thr lys
gly
481/161

gtc acc gtc ctg aat cta cca aca ggg ttc gac aaa cca tac gtc cgc cta gag gac
gag
val thr val leu asn leu pro thr gly phe asp lys pro tyr val arg leu glu asp
glu
541/181

aca ccc cag ggt ctc cag tca atg aac ggg gcc agg atg agg tgc aca gct cca att
gca
thr pro gln gly leu gln ser met asn gly ala arg met arg cys thr ala ala ie
ala
601/201

cca cgg agg tac gag atc gac ctc cca tcc caa agc cta ccc ccc gtt cct ggg aca
gga
pro arg arg tyr glu ile asp leu pro ser gln ser leu pro pro val pro ala trp
gly
661/221

acc ctc acc act ctc tac gag gga aac gcc gac atc gtc agc tcc aca aca gtc acg
gga
thr leu thr thr leu tyr glu gly asn ala asp ile val ser ser thr thr val thr
gly
721/241

gac ala aac ttc agt ctg gca gaa cga ccc gca aac gag acc agg ttc gac tc cag
ctg
asp ile asn phe ser leu ala glu arg pro ala asn glu thr arg phe asp pro gln
l u

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Appendix 4

The T3 protein sequence is:

FACKTANGTAIPIGGGSANVYVNLAPVVNVGQNLVWLSTQIFCHNDYPETITDYVTLQRGSA
SYPFPTTSETPRVVYNSRTDKPWPVALYLTPVSSAGGVAIKAGSLIAVLILRQTNNYNSDDFQ
CDVSA

The T7 protein sequence is:

FACKTANGTAIPIGGGSANVYVNLAPVVNVGQNLVWLSTQIFCHNDYPETITDYVTLQRGSA
SYPFPTTSETPRVVYNSRTDKPWPVALYLTPVSSAGGVAIKAGSLIAVLILRQTNNYNSDDFQ
CDVSARDVTVTLPDYRGSVPIPLTVYCAKSQNLGYLSGTHADAGNSIFTNTASFSPAQGVG
GAVGTSAVSLGLTANYARTGGQVTAGNVQSIIGVTFVYQ

2000.04.06